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STANDAGE, SCOTT

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ANTIBIOTIC C-1027

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<140> 09/478,188
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<150> 60/115,434
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23

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<220>
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<223> s is g or c

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27

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<223> v is a or g

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<223> n is a, c, g, or t

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<223> y is t or c

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<223> b is c or g

<220>

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<223> v is a or g

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18

<210> 105

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<222> (4)..(4)

<223> s is g or c

<220>

<221> misc_feature

<222> (7)..(7)

<223> r is a or g

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<222> (10)..(10)

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<222> (13)..(13)

<223> n is a, c, g, or t

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<222> (16)..(16)

<223> r is a or g

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<223> s is g or c

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<223> s is g or c

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26

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<222> (3)..(3)

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<223> s is g or c

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<222> (21)..(21)

<223> s is g or c

<220>

<221> misc_feature

<222> (24)..(24)

<223> s is g or c

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<222> (12)..(12)

<223> s is g or c

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20

<210> 112

<211> 3035

<212> DNA

<213> Streptomyces globisporus

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<222> (1143)..(2705)

<223> sgcB gene

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Met Arg Met Leu Val

	1	5	
acg ggc gga gcg ggt ttc atc ggc tgc cag ttc gtg cgg gcc aca ctg			163
Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe Val Arg Ala Thr Leu	10	15	20
cac ggc gag ctg ccg ggt tcc gag gac gcc cgg gtg acg gtc ctg gac			211
His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg Val Thr Val Leu Asp	25	30	35
aag ctg acg tac tcc ggc aat ccg gcc aac ctc acc tcc gtc gcg gcc			259
Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu Thr Ser Val Ala Ala	40	45	50
cat ccg cgg tac acc ttc gtc cag ggc gac acc gtc gac ccg cgc gtc			307
His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr Val Asp Pro Arg Val	55	60	65
gtc gac gag gtg gtc gcc ggc cac gac gtc atc gtc cac ttc gcg gcg			355
Val Asp Glu Val Val Ala Gly His Asp Val Ile Val His Phe Ala Ala	70	75	85
gag tgc cac gtg gac cgc tgc atc gac acc gcc acc cgg ttc gtc acg			403
Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala Thr Arg Phe Val Thr	90	95	100
acc aac gtg ctc ggg acc cag acg ctg ctg gaa gcg gct ctc cgg cac			451
Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu Ala Ala Leu Arg His	105	110	115
ggg gtc ggc cgg ttc gtg cac gtg tgc acc gac gag gtc tac ggg tgc			499
Gly Val Gly Arg Phe Val His Val Ser Thr Asp Glu Val Tyr Gly Ser	120	125	130
atc gcc tcc ggc tca tgg acc gag gac acc ccg ctc gcc ccc aac gtc			547
Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro Leu Ala Pro Asn Val	135	140	145
ccc tac gcg gcg tgc aag gcg ggt tgc gac ctg atg gcg ctc gcc tgg			595
Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu Met Ala Leu Ala Trp	150	155	165
cac cgc acc cgg ggc ctg gac gtc gtc gtc acc cgg tgc acc aac aac			643
His Arg Thr Arg Gly Leu Asp Val Val Thr Arg Cys Thr Asn Asn	170	175	180
tac ggt ccc tac cag tac ccc gag aag gtg atc ccg ctc ttc gtc acc			691
Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile Pro Leu Phe Val Thr	185	190	195
aac atc ctc gac ggc ttg cgg gtg ccc ctg tac ggg gac ggc gcc cac			739
Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr Gly Asp Gly Ala His	200	205	210
cgc cgg gac tgg ctg cac gtg tcc gac cac tgc cgg gcc atc cag atg			787
Arg Arg Asp Trp Leu His Val Ser Asp His Cys Arg Ala Ile Gln Met	215	220	225

gtc atg aac tcc ggc cgg gcc ggg gag gtc tac cac atc ggc ggc ggc	835
Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr His Ile Gly Gly Gly	
230 235 240 245	
acc gaa ctc tcc aac gag gaa ctc acc ggc ctg ttg ctc acg gcg tgc	883
Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu Leu Leu Thr Ala Cys	
250 255 260	
ggc acc gac tgg tcc tgc gtg gac cgg gtg gcc gac cgg cag ggg cac	931
Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala Asp Arg Gln Gly His	
265 270 275	
gac cgc cgc tac tgc ctc gac atc acg aag atc cgg cag gaa ctg ggc	979
Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile Arg Gln Glu Leu Gly	
280 285 290	
tac gag ccc ctg gtc gcc ttc gag gac ggc ctg gcc gcg acg gtg aag	1027
Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu Ala Ala Thr Val Lys	
295 300 305	
tgg tac cac gag aac cgt tgc tgg tgg cag ccg ctg aag gaa gcg gcc	1075
Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro Leu Lys Glu Ala Ala	
310 315 320 325	
ggc ctc ctg gac gcc gtc ggc tgacggcagc caccgctagg aacaccccag	1126
Gly Leu Leu Asp Ala Val Gly	
330	
gaaaggagcc acctcc gtg aca gca gtc aag gag ccg acg tcc cgc gca gga	1178
Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly	
335 340	
cgg cgg gag tgg atc gct ctc gtc gtc ctc tcc ttg ccc acg atg ctg	1226
Arg Arg Glu Trp Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu	
345 350 355 360	
ttg atg ctg gac atc aac gtc ctc atg ctg gcc ttg ccg cag ttg agc	1274
Leu Met Leu Asp Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser	
365 370 375	
gag gat ctc ggc gcg agc agc acg caa cag ctg tgg atc acc gac atc	1322
Glu Asp Leu Gly Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile	
380 385 390	
tac gga ttc gcg atc gcc ggc ttc ctg gtg acc atg ggc acc ctc ggc	1370
Tyr Gly Phe Ala Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly	
395 400 405	
gac cgg atc ggc cgc cgc agg ctc ctg ctc ggg ggc gcg gcc gtc ttc	1418
Asp Arg Ile Gly Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe	
410 415 420	
gcg gtc gtg tcc gtc gtc gcc gcg ttc tcc gac agc gcg gcg atg ctc	1466
Ala Val Val Ser Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu	
425 430 435 440	

gtc gtc agc cgc gcc gtg ctc ggc gtc gcc ggg gcc acg gtg atg ccc	1514
Val Val Ser Arg Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro	
445 450 455	
tcg acg ctc gcg ctc atc agc aac atg ttc gag gac ccc aag gag cgg	1562
Ser Thr Leu Ala Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg	
460 465 470	
ggc acc gcc atc gcc atg tgg gcg agc gcc atg atg gcc gga gtc gcc	1610
Gly Thr Ala Ile Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala	
475 480 485	
ctc ggg ccc gcc gtc gcc gcc ctg gtc ctc gcc gcg ttc tgg tgg gga	1658
Leu Gly Pro Ala Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly	
490 495 500	
tcg gtg ttc ctc atc gcc gtt ccg gtg atg ctg ctg gtg gtg gtc acc	1706
Ser Val Phe Leu Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr	
505 510 515 520	
ggc ccc gtg ctg ctc acc gag tcc cgc gac ccg gac gcc gga cgg ctg	1754
Gly Pro Val Leu Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu	
525 530 535	
gac ctg ctg agc gcg ggg ctc tcc ctc gcg acc gtg ctg ccg gtg atc	1802
Asp Leu Leu Ser Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile	
540 545 550	
tac gga ctg aag gag ctg gcc cgg acc ggg tgg gac ccg ctc gcc gcc	1850
Tyr Gly Leu Lys Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala	
555 560 565	
ggc gcg gtg gtc ctc gcc gtg atc ttc gcc gcg ctg ttc gtc cag cgc	1898
Gly Ala Val Val Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg	
570 575 580	
cag cgg cgg ttg gcc gac ccc atg ctg gac ctc gcc ctc ttc gcc gac	1946
Gln Arg Arg Leu Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp	
585 590 595 600	
cgc acc ctg cgg gcg ggt ctg acg gtc agt ctg gtc aac gcc gtc atc	1994
Arg Thr Leu Arg Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile	
605 610 615	
atg ggc ggg acc gga ctg atg gtc gcc ctg tac ctc cag acg atc gcc	2042
Met Gly Gly Thr Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala	
620 625 630	
ggt cac tcc ccg ttg gcc gcc ggg ctg tgg ctg ctg atc ccg gcc tgc	2090
Gly His Ser Pro Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys	
635 640 645	
atg ctc gtc gtg gcc gta cag ctg tcg aac ctg ctg gcc cag cgg atg	2138
Met Leu Val Val Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met	
650 655 660	
ccc cct tcc cgg gtg ctg ctg ggg gga ctg ctg atc gcg gcc gtc gga	2186

Pro	Pro	Ser	Arg	Val	Leu	Leu	Gly	Gly	Leu	Leu	Ile	Ala	Ala	Val	Gly	
665					670					675					680	
cag	ctc	ctg	atc	acc	cag	gtg	gac	acc	gag	gac	acc	gcc	ctc	ctc	atc	2234
Gln	Leu	Leu	Ile	Thr	Gln	Val	Asp	Thr	Glu	Asp	Thr	Ala	Leu	Leu	Ile	
				685					690					695		
gcg	gcc	acc	acc	ctg	atc	tac	ttc	ggc	gcc	tca	ccg	gtg	ggg	ccg	atc	2282
Ala	Ala	Thr	Thr	Leu	Ile	Tyr	Phe	Gly	Ala	Ser	Pro	Val	Gly	Pro	Ile	
				700				705					710			
acc	acg	ggc	gcg	atc	atg	gga	gcc	gcg	ccc	ccg	gag	aag	gcg	ggg	gcc	2330
Thr	Thr	Gly	Ala	Ile	Met	Gly	Ala	Ala	Pro	Pro	Glu	Lys	Ala	Gly	Ala	
		715					720					725				
gcc	tgc	tgc	ctg	tcc	gcc	acc	ggc	ggc	gag	ttc	gga	gtg	gcg	ctc	ggc	2378
Ala	Ser	Ser	Leu	Ser	Ala	Thr	Gly	Gly	Glu	Phe	Gly	Val	Ala	Leu	Gly	
	730					735					740					
atc	gcg	ggc	ctg	ggg	agt	ctg	ggc	acc	gtc	gtg	tac	agc	gcc	ggg	gtc	2426
Ile	Ala	Gly	Leu	Gly	Ser	Leu	Gly	Thr	Val	Val	Tyr	Ser	Ala	Gly	Val	
745					750				755					760		
gag	gtg	ccg	gac	gcg	gcc	ggg	ccc	gcc	gac	gcc	gac	gcc	gcg	cag	gag	2474
Glu	Val	Pro	Asp	Ala	Ala	Gly	Pro	Ala	Asp	Ala	Asp	Ala	Ala	Gln	Glu	
				765				770						775		
agc	atc	gcc	ggc	gcc	ctg	cac	acg	gcc	ggg	cag	ctg	gca	ccg	ggc	agc	2522
Ser	Ile	Ala	Gly	Ala	Leu	His	Thr	Ala	Gly	Gln	Leu	Ala	Pro	Gly	Ser	
			780					785					790			
gcc	gac	gcc	ctg	ctg	gac	tcc	gcg	cgc	gcg	gcc	ttc	acc	agc	ggc	gtg	2570
Ala	Asp	Ala	Leu	Leu	Asp	Ser	Ala	Arg	Ala	Ala	Phe	Thr	Ser	Gly	Val	
		795					800					805				
cag	tcc	gtc	gcc	gcc	gtc	tgc	gcc	gtg	ttc	tcc	ctg	gcg	ctc	gcc	gtc	2618
Gln	Ser	Val	Ala	Ala	Val	Cys	Ala	Val	Phe	Ser	Leu	Ala	Leu	Ala	Val	
	810					815					820					
ctc	atc	ggc	acc	cgg	ctg	cgg	gac	att	tcc	gcg	atg	gac	cac	ggg	cac	2666
Leu	Ile	Gly	Thr	Arg	Leu	Arg	Asp	Ile	Ser	Ala	Met	Asp	His	Gly	His	
825					830				835					840		
ggc	gag	gaa	ccg	gcc	gag	aac	gac	gct	caa	ccg	gcc	aca	tgagcgcact			2715
Gly	Glu	Glu	Pro	Ala	Glu	Asn	Asp	Ala	Gln	Pro	Ala	Thr				
				845				850								
tccggagatg	caacggccgc	cgtcgaggta	tgaggatcac	cttcgggggt	gcacctgcac											2775
ggcaacggag	gcgtagtgga	gtactggaac	agcacggcgg	agaccatgcc	ccgccaggaa											2835
ctcgaacagt	ggaagtggcg	caggctccag	gccgccatgg	accacgccag	aaggctttcg											2895
cccttctggc	gggaacgact	ccccgagaac	atcacctcca	tggcgggacta	cgcggcgcgg											2955
gtgcctctcc	tgcgcaaggc	cgacctcttc	gccgcggaag	ccgcgtctcc	cccttacggc											3015

acctggccct cgctggatcc

3035

<210> 113

<211> 332

<212> PRT

<213> Streptomyces globisporus

<220>

<223> sgCA

<400> 113

Met Arg Met Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe
1 5 10 15

Val Arg Ala Thr Leu His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg
20 25 30

Val Thr Val Leu Asp Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu
35 40 45

Thr Ser Val Ala Ala His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr
50 55 60

Val Asp Pro Arg Val Val Asp Glu Val Val Ala Gly His Asp Val Ile
65 70 75 80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala
85 90 95

Thr Arg Phe Val Thr Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu
100 105 110

Ala Ala Leu Arg His Gly Val Gly Arg Phe Val His Val Ser Thr Asp
115 120 125

Glu Val Tyr Gly Ser Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro
130 135 140

Leu Ala Pro Asn Val Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu
145 150 155 160

Met Ala Leu Ala Trp His Arg Thr Arg Gly Leu Asp Val Val Val Thr
165 170 175

Arg Cys Thr Asn Asn Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile
180 185 190

Pro Leu Phe Val Thr Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr
195 200 205

Gly Asp Gly Ala His Arg Arg Asp Trp Leu His Val Ser Asp His Cys
210 215 220

Arg Ala Ile Gln Met Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr
225 230 235 240

Val	Gly	Gly	Leu	Val	Leu	Ala	Ala	Phe	Trp	Trp	Gly	Ser	Val	Phe	Leu	165	170	175
Ile	Ala	Val	Pro	Val	Met	Leu	Leu	Val	Val	Val	Thr	Gly	Pro	Val	Leu	180	185	190
Leu	Thr	Glu	Ser	Arg	Asp	Pro	Asp	Ala	Gly	Arg	Leu	Asp	Leu	Leu	Ser	195	200	205
Ala	Gly	Leu	Ser	Leu	Ala	Thr	Val	Leu	Pro	Val	Ile	Tyr	Gly	Leu	Lys	210	215	220
Glu	Leu	Ala	Arg	Thr	Gly	Trp	Asp	Pro	Leu	Ala	Ala	Gly	Ala	Val	Val	225	230	240
Leu	Gly	Val	Ile	Phe	Gly	Ala	Leu	Phe	Val	Gln	Arg	Gln	Arg	Arg	Leu	245	250	255
Ala	Asp	Pro	Met	Leu	Asp	Leu	Gly	Leu	Phe	Ala	Asp	Arg	Thr	Leu	Arg	260	265	270
Ala	Gly	Leu	Thr	Val	Ser	Leu	Val	Asn	Ala	Val	Ile	Met	Gly	Gly	Thr	275	280	285
Gly	Leu	Met	Val	Ala	Leu	Tyr	Leu	Gln	Thr	Ile	Ala	Gly	His	Ser	Pro	290	295	300
Leu	Ala	Ala	Gly	Leu	Trp	Leu	Leu	Ile	Pro	Ala	Cys	Met	Leu	Val	Val	305	310	315
Gly	Val	Gln	Leu	Ser	Asn	Leu	Leu	Ala	Gln	Arg	Met	Pro	Pro	Ser	Arg	325	330	335
Val	Leu	Leu	Gly	Gly	Leu	Leu	Ile	Ala	Ala	Val	Gly	Gln	Leu	Leu	Ile	340	345	350
Thr	Gln	Val	Asp	Thr	Glu	Asp	Thr	Ala	Leu	Leu	Ile	Ala	Ala	Thr	Thr	355	360	365
Leu	Ile	Tyr	Phe	Gly	Ala	Ser	Pro	Val	Gly	Pro	Ile	Thr	Thr	Gly	Ala	370	375	380
Ile	Met	Gly	Ala	Ala	Pro	Pro	Glu	Lys	Ala	Gly	Ala	Ala	Ser	Ser	Leu	385	390	395
Ser	Ala	Thr	Gly	Gly	Glu	Phe	Gly	Val	Ala	Leu	Gly	Ile	Ala	Gly	Leu	405	410	415
Gly	Ser	Leu	Gly	Thr	Val	Val	Tyr	Ser	Ala	Gly	Val	Glu	Val	Pro	Asp	420	425	430
Ala	Ala	Gly	Pro	Ala	Asp	Ala	Asp	Ala	Ala	Gln	Glu	Ser	Ile	Ala	Gly	435	440	445
Ala	Leu	His	Thr	Ala	Gly	Gln	Leu	Ala	Pro	Gly	Ser	Ala	Asp	Ala	Leu	450	455	460

195					200					205					
Gly	Asp	Gly	Leu	Asn	Val	Arg	Asp	Trp	Leu	His	Val	Thr	Asp	His	Cys
210						215					220				
Arg	Gly	Ile	Gln	Leu	Val	Ala	Glu	Ser	Gly	Arg	Ala	Gly	Glu	Ile	Tyr
225					230					235					240
Asn	Ile	Gly	Gly	Gly	Thr	Glu	Leu	Thr	Asn	Lys	Glu	Leu	Thr	Glu	Arg
				245					250					255	
Val	Leu	Glu	Leu	Met	Gly	Gln	Asp	Trp	Ser	Met	Val	Gln	Pro	Val	Thr
			260					265					270		
Asp	Arg	Lys	Gly	His	Asp	Arg	Arg	Tyr	Ser	Val	Asp	His	Thr	Lys	Ile
		275					280					285			
Ser	Glu	Glu	Leu	Gly	Tyr	Glu	Pro	Val	Val	Pro	Phe	Glu	Arg	Gly	Leu
	290					295					300				
Ala	Glu	Thr	Ile	Glu	Trp	Tyr	Arg	Asp	Asn	Arg	Ala	Trp	Trp	Glu	Pro
305					310					315					320
Leu	Lys	Ser	Ala	Pro	Asp	Gly	Gly	Lys							
				325											

<210> 116

<211> 333

<212> PRT

<213> Streptomyces fradiae

<400> 116

Met	Arg	Val	Leu	Val	Thr	Gly	Gly	Ala	Gly	Phe	Ile	Gly	Ser	His	Phe
1				5					10					15	
Thr	Gly	Gln	Leu	Leu	Thr	Gly	Ala	Tyr	Pro	Asp	Leu	Gly	Ala	Thr	Arg
		20					25						30		
Thr	Val	Val	Leu	Asp	Lys	Leu	Thr	Tyr	Ala	Gly	Asn	Pro	Ala	Asn	Leu
		35					40					45			
Glu	His	Val	Ala	Gly	His	Pro	Asp	Leu	Glu	Phe	Val	Arg	Gly	Asp	Ile
	50					55					60				
Ala	Asp	His	Gly	Trp	Trp	Arg	Arg	Leu	Met	Glu	Gly	Val	Gly	Leu	Val
65					70					75					80
Val	His	Phe	Ala	Ala	Glu	Ser	His	Val	Asp	Arg	Ser	Ile	Glu	Ser	Ser
			85						90					95	
Glu	Ala	Phe	Val	Arg	Thr	Asn	Val	Glu	Gly	Thr	Arg	Val	Leu	Leu	Gln
		100						105					110		
Ala	Ala	Val	Asp	Ala	Gly	Val	Gly	Arg	Phe	Val	His	Ile	Ser	Thr	Asp
		115					120					125			

Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Pro Glu Asp His Pro
 130 135 140
 Val Ala Pro Asn Ser Pro Tyr Ala Ala Thr Lys Lys Ala Ser Asp Leu
 145 150 155 160
 Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Asp Val Arg Val Thr
 165 170 175
 Arg Cys Ser Asn Asn Tyr Gly Pro Arg Gln Tyr Pro Glu Lys Ala Val
 180 185 190
 Pro Leu Phe Thr Thr Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr
 195 200 205
 Gly Asp Gly Gly Asn Thr Arg Glu Trp Leu His Val Asp Asp His Cys
 210 215 220
 Arg Gly Val Ala Leu Val Gly Ala Gly Gly Arg Pro Gly Val Ile Tyr
 225 230 235 240
 Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Ala Glu Leu Thr Asp Arg
 245 250 255
 Ile Leu Glu Leu Cys Gly Ala Asp Arg Ser Ala Leu Arg Arg Val Ala
 260 265 270
 Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
 275 280 285
 Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
 290 295 300
 Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
 305 310 315 320
 Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
 325 330

<210> 117

<211> 331

<212> PRT

<213> Streptomyces argillaceus

<400> 117

Met Thr Thr Thr Ser Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly
 1 5 10 15
 Ser His Tyr Val Arg Thr Leu Leu Gly Pro Arg Gly Val Pro Asp Val
 20 25 30
 Thr Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Thr Leu Thr Asn
 35 40 45
 Leu Ala Glu Val Ser Asp Ser Asp Arg Phe Arg Phe Val Arg Gly Asp
 50 55 60

Ile	Cys	Asp	Ala	Pro	Leu	Val	Asp	Asp	Leu	Leu	Ala	Val	His	Asp	Gln	
65					70					75					80	
Val	Val	His	Phe	Ala	Ala	Glu	Ser	His	Val	Asp	Arg	Ser	Ile	Leu	Gly	
			85						90					95		
Ala	Ala	Asp	Phe	Val	Arg	Thr	Asn	Val	Thr	Gly	Thr	Gln	Thr	Leu	Leu	
			100					105					110			
Asp	Ala	Ala	Leu	Arg	Gln	Gly	Ile	Glu	Thr	Phe	Val	His	Ile	Ser	Thr	
		115					120					125				
Asp	Glu	Val	Tyr	Gly	Ser	Ile	Asp	Ala	Gly	Ser	Trp	Pro	Glu	Thr	Ala	
	130					135					140					
Pro	Val	Ser	Pro	Asn	Ser	Leu	Tyr	Ser	Ala	Ala	Lys	Ala	Ser	Ser	Asp	
145					150					155					160	
Leu	Val	Ala	Leu	Ala	Tyr	His	Arg	Thr	His	Gly	Leu	Asp	Val	Arg	Val	
			165						170					175		
Thr	Arg	Cys	Ser	Asn	Asn	Tyr	Gly	Ser	His	Gln	Phe	Pro	Glu	Lys	Val	
			180					185					190			
Ile	Pro	Leu	Phe	Val	Thr	Ser	Leu	Leu	Asp	Gly	Arg	Glu	Val	Pro	Leu	
		195					200					205				
Tyr	Gly	Asp	Gly	Thr	Asn	Val	Arg	Asp	Trp	Leu	His	Val	Asp	Asp	His	
	210					215					220					
Val	Arg	Ala	Ile	Glu	Leu	Val	Arg	Thr	Gly	Gly	Arg	Ala	Gly	Glu	Val	
225					230					235					240	
Tyr	Asn	Ile	Gly	Gly	Gly	Thr	Glu	Leu	Ser	Asn	Lys	Glu	Leu	Thr	Gln	
			245						250					255		
Leu	Leu	Leu	Asp	Ala	Cys	Gly	Ala	Gly	Trp	Asp	Arg	Val	Arg	Tyr	Val	
			260					265					270			
Thr	Asp	Arg	Lys	Gly	His	Asp	Arg	Arg	Tyr	Ser	Val	Asp	Cys	Thr	Lys	
		275					280					285				
Ile	Arg	Arg	Glu	Leu	Gly	Tyr	Arg	Pro	Ala	Arg	Glu	Phe	Gly	Asp	Ala	
	290					295					300					
Leu	Ala	Glu	Thr	Val	Ala	Trp	Tyr	Arg	His	His	Arg	Ala	Trp	Trp	Glu	
305					310					315					320	
Pro	Leu	Thr	Arg	Ala	Tyr	Gly	Ala	Val	Ala	Ala						
				325					330							

<210> 118

<211> 6

<212> PRT

<213> Artificial Sequence .

<220>

<223> Description of Artificial Sequence: 6-His tag

<400> 118

His His His His His His
1 5

<210> 119

<211> 256

<212> PRT

<213> Artificial

<220>

<223> Computed consensus sequence.

<400> 119

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
1 5 10 15

Val Arg Ile Leu Gly Pro Ala Val Val Leu Asp Lys Leu Thr Tyr Ala
20 25 30

Gly Asn Asn Leu Val Ala Pro Arg Phe Phe Val Arg Gly Asp Ile Asp
35 40 45

Val Val Glu Val Met Asp Val Val Val His Phe Ala Ala Glu Ser His
50 55 60

Val Asp Arg Ser Ile Ala Phe Val Thr Asn Val Gly Thr Asn Thr Leu
65 70 75 80

Leu Ala Ala Leu Gly Val Lys Phe Val His Val Ser Thr Asp Glu Val
85 90 95

Tyr Gly Ser Ile Gly Ser Trp Pro Glu Asp Pro Leu Pro Asn Ser Pro
100 105 110

Tyr Ala Lys Ala Gly Ser Asp Leu Ile Ala Leu Ala Tyr His Arg Thr
115 120 125

His Gly Leu Asp Val Val Thr Arg Cys Ser Asn Asn Tyr Gly Pro Gln
130 135 140

Phe Pro Glu Lys Val Leu Pro Leu Phe Ile Thr Asn Leu Leu Asp Gly
145 150 155 160

Val Pro Leu Tyr Gly Asp Gly Asn Arg Asp Trp Leu His Val Asp His
165 170 175

Cys	Arg	Gly	Ile	Leu	Val	Gly	Arg	Ala	Gly	Glu	Ile	Tyr	Asn	Ile	Gly
			180					185					190		
Gly	Gly	Thr	Glu	Leu	Thr	Asn	Glu	Leu	Thr	Val	Leu	Glu	Cys	Gly	Asp
		195					200					205			
Trp	Ser	Val	Val	Asp	Arg	Gly	His	Asp	Arg	Arg	Tyr	Ser	Val	Asp	Thr
	210					215					220				
Lys	Ile	Arg	Glu	Leu	Gly	Tyr	Pro	Phe	Glu	Gly	Leu	Ala	Thr	Val	Trp
225					230					235					240
Tyr	Arg	Asp	Asn	Arg	Ala	Trp	Trp	Glu	Leu	Pro	Leu	Lys	Ala	Gly	Gly
				245					250					255	